PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION   *US/09/451,939*

DATE: 12/19/1999
TIME: 04:18:14

INPUT SET: S34265.raw

> This Raw Listing contains the General
> Information Section and up to the first 5 pages.

```
 1                            SEQUENCE LISTING              .
 2
 3   (1)    General Information:
 4
 5        (i) APPLICANTS: Miao, Ningning
 6                       Wang, Monica
 7                       Mahanthappa, Nagesh K.
 8                       Jin, Ping
 9                       Pang, Kevin
10
11       (ii) TITLE OF INVENTION: Method of Treating Dopaminergic and
12            GABA-nergic Disorders
13
14      (iii) NUMBER OF SEQUENCES: 22
15
16       (iv) CORRESPONDENCE ADDRESS:
17            (A) ADDRESSEE: FOLEY, HOAG & ELIOT LLP
18            (B) STREET: ONE POST OFFICE SQUARE
19            (C) CITY: Boston
20            (D) STATE: MA
21            (E) COUNTRY: USA
22            (F) ZIP: 02109
23
24       (v) COMPUTER READABLE FORM:
25            (A) MEDIUM TYPE: Floppy disk
26            (B) COMPUTER: IBM PC compatible
27            (C) OPERATING SYSTEM: PC-DOS/MS-DOS
28            (D) SOFTWARE: AscII (text)
29
30       (vi) CURRENT APPLICATION DATA:
31            (A) APPLICATION NUMBER:
32            (B) FILING DATE:
33            (C) CLASSIFICATION:
34
35      (vii) PRIOR APPLICATION DATA:
36            (A) APPLICATION NUMBER: US 08/900,220
37            (B) FILING DATE: 24-JUL-1997
38
39     (viii) ATTORNEY/AGENT INFORMATION:
40            (A) NAME: Vincent, Matthew P.
41            (B) REGISTRATION NUMBER: 36,709
42            (C) REFERENCE/DOCKET NUMBER: ONV-044.01
43
44       (ix) TELECOMMUNICATION INFORMATION:
45            (A) TELEPHONE: (617) 832-1000
46            (B) TELEFAX: (617) 832-7000
```

```
47
48
49      (2) INFORMATION FOR SEQ ID NO:1:
50          (i) SEQUENCE CHARACTERISTICS:
51              (A) LENGTH: 1277 base pairs
52              (B) TYPE: nucleic acid
53              (C) STRANDEDNESS: both
54              (D) TOPOLOGY: linear
55
56          (ii) MOLECULE TYPE: cDNA
57
58          (ix) FEATURE:
59              (A) NAME/KEY: CDS
60              (B) LOCATION: 1..1275
61
62          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
63
64      ATG GTC GAA ATG CTG CTG TTG ACA AGA ATT CTC TTG GTG GGC TTC ATC         48
65      Met Val Glu Met Leu Leu Leu Thr Arg Ile Leu Leu Val Gly Phe Ile
66       1               5                   10                  15
67
68      TGC GCT CTT TTA GTC TCC TCT GGG CTG ACT TGT GGA CCA GGC AGG GGC         96
69      Cys Ala Leu Leu Val Ser Ser Gly Leu Thr Cys Gly Pro Gly Arg Gly
70                   20                  25                  30
71
72      ATT GGA AAA AGG AGG CAC CCC AAA AAG CTG ACC CCG TTA GCC TAT AAG        144
73      Ile Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys
74                   35                  40                  45
75
76      CAG TTT ATT CCC AAT GTG GCA GAG AAG ACC CTA GGG GCC AGT GGA AGA        192
77      Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg
78           50                  55                  60
79
80      TAT GAA GGG AAG ATC ACA AGA AAC TCC GAG AGA TTT AAA GAA CTA ACC        240
81      Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr
82       65                  70                  75                  80
83
84      CCA AAT TAC AAC CCT GAC ATT ATT TTT AAG GAT GAA GAG AAC ACG GGA        288
85      Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly
86                   85                  90                  95
87
88      GCT GAC AGA CTG ATG ACT CAG CGC TGC AAG GAC AAG CTG AAT GCC CTG        336
89      Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu
90                   100                 105                 110
91
92      GCG ATC TCG GTG ATG AAC CAG TGG CCC GGG GTG AAG CTG CGG GTG ACC        384
93      Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr
94                   115                 120                 125
95
96      GAG GGC TGG GAC GAG GAT GGC CAT CAC TCC GAG GAA TCG CTG CAC TAC        432
97      Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr
98                   130                 135                 140
99
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INPUT SET: S34265.raw

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101  Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys
102  145             150             155             160

103
104  TAC GGA ATG CTG GCC CGC CTC GCC GTC GAG GCC GGC TTC GAC TGG GTC      528
105  Tyr Gly Met Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val
106  165             170             175

107
108  TAC TAC GAG TCC AAG GCG CAC ATC CAC TGC TCC GTC AAA GCA GAA AAC      576
109  Tyr Tyr Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn
110  180             185             190

111
112  TCA GTG GCA GCG AAA TCA GGA GGC TGC TTC CCT GGC TCA GCC ACA GTG      624
113  Ser Val Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val
114  195             200             205

115
116  CAC CTG GAG CAT GGA GGC ACC AAG CTG GTG AAG GAC CTG AGC CCT GGG      672
117  His Leu Glu His Gly Gly Thr Lys Leu Val Lys Asp Leu Ser Pro Gly
118  210             215             220

119
120  GAC CGC GTG CTG GCT GCT GAC GCG GAC GGC CGG CTG CTC TAC AGT GAC      720
121  Asp Arg Val Leu Ala Ala Asp Ala Asp Gly Arg Leu Leu Tyr Ser Asp
122  225             230             235             240

123
124  TTC CTC ACC TTC CTC GAC CGG ATG GAC AGC TCC CGA AAG CTC TTC TAC      768
125  Phe Leu Thr Phe Leu Asp Arg Met Asp Ser Ser Arg Lys Leu Phe Tyr
126  245             250             255

127
128  GTC ATC GAG ACG CGG CAG CCC CGG GCC CGG CTG CTA CTG ACG GCG GCC      816
129  Val Ile Glu Thr Arg Gln Pro Arg Ala Arg Leu Leu Leu Thr Ala Ala
130  260             265             270

131
132  CAC CTG CTC TTT GTG GCC CCC CAG CAC AAC CAG TCG GAG GCC ACA GGG      864
133  His Leu Leu Phe Val Ala Pro Gln His Asn Gln Ser Glu Ala Thr Gly
134  275             280             285

135
136  TCC ACC AGT GGC CAG GCG CTC TTC GCC AGC AAC GTG AAG CCT GGC CAA      912
137  Ser Thr Ser Gly Gln Ala Leu Phe Ala Ser Asn Val Lys Pro Gly Gln
138  290             295             300

139
140  CGT GTC TAT GTG CTG GGC GAG GGC GGG CAG CAG CTG CTG CCG GCG TCT      960
141  Arg Val Tyr Val Leu Gly Glu Gly Gly Gln Gln Leu Leu Pro Ala Ser
142  305             310             315             320

143
144  GTC CAC AGC GTC TCA TTG CGG GAG GAG GCG TCC GGA GCC TAC GCC CCA     1008
145  Val His Ser Val Ser Leu Arg Glu Glu Ala Ser Gly Ala Tyr Ala Pro
146  325             330             335

147
148  CTC ACC GCC CAG GGC ACC ATC CTC ATC AAC CGG GTG TTG GCC TCC TGC     1056
149  Leu Thr Ala Gln Gly Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys
150  340             345             350

151
152  TAC GCC GTC ATC GAG GAG CAC AGT TGG GCC CAT TGG GCC TTC GCA CCA     1104
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INPUT SET: S34265.raw

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153    Tyr Ala Val Ile Glu Glu His Ser Trp Ala His Trp Ala Phe Ala Pro
154            355             360             365

155
156    TTC CGC TTG GCT CAG GGG CTG CTG GCC GCC CTC TGC CCA GAT GGG GCC        1152
157    Phe Arg Leu Ala Gln Gly Leu Leu Ala Ala Leu Cys Pro Asp Gly Ala
158            370             375             380

159
160    ATC CCT ACT GCC GCC ACC ACC ACC ACT GGC ATC CAT TGG TAC TCA CGG        1200
161    Ile Pro Thr Ala Ala Thr Thr Thr Thr Gly Ile His Trp Tyr Ser Arg
162    385             390             395             400
163    CTC CTC TAC CGC ATC GGC AGC TGG GTG CTG GAT GGT GAC GCG CTG CAT        1248
164    Leu Leu Tyr Arg Ile Gly Ser Trp Val Leu Asp Gly Asp Ala Leu His
165            405             410             415
166
167    CCG CTG GGC ATG GTG GCA CCG GCC AGC TG                                 1277
168    Pro Leu Gly Met Val Ala Pro Ala Ser
169            420             425

170
171
172    (2) INFORMATION FOR SEQ ID NO:2:
173
174        (i) SEQUENCE CHARACTERISTICS:
175            (A) LENGTH: 1190 base pairs
176            (B) TYPE: nucleic acid
177            (C) STRANDEDNESS: both
178            (D) TOPOLOGY: linear
179
180        (ii) MOLECULE TYPE: cDNA
181
182        (ix) FEATURE:
183            (A) NAME/KEY: CDS
184            (B) LOCATION: 1..1191
185
186        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
187
188    ATG GCT CTG CCG GCC AGT CTG TTG CCC CTG TGC TGC TTG GCA CTC TTG        48
189    Met Ala Leu Pro Ala Ser Leu Leu Pro Leu Cys Cys Leu Ala Leu Leu
190    1               5               10              15
191
192    GCA CTA TCT GCC CAG AGC TGC GGG CCG GGC CGA GGA CCG GTT GGC CGG        96
193    Ala Leu Ser Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg
194            20              25              30
195
196    CGG CGT TAT GTG CGC AAG CAA CTT GTG CCT CTG CTA TAC AAG CAG TTT        144
197    Arg Arg Tyr Val Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe
198            35              40              45
199
200    GTG CCC AGT ATG CCC GAG CGG ACC CTG GGC GCG AGT GGG CCA GCG GAG        192
201    Val Pro Ser Met Pro Glu Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu
202    50              55              60
203
204    GGG AGG GTA ACA AGG GGG TCG GAG CGC TTC CGG GAC CTC GTA CCC AAC        240
205    Gly Arg Val Thr Arg Gly Ser Glu Arg Phe Arg Asp Leu Val Pro Asn
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INPUT SET: S34265.raw

```
206    65                    70                    75                    80
207
208    TAC AAC CCC GAC ATA ATC TTC AAG GAT GAG GAG AAC AGC GGC GCA GAC        288
209    Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp
210                    85                    90                    95
211
212    CGC CTG ATG ACA GAG CGT TGC AAA GAG CGG GTG AAC GCT CTA GCC ATC        336
213    Arg Leu Met Thr Glu Arg Cys Lys Glu Arg Val Asn Ala Leu Ala Ile
214                    100                   105                   110
215
216    GCG GTG ATG AAC ATG TGG CCC GGA GTA CGC CTA CGT GTG ACT GAA GGC        384
217    Ala Val Met Asn Met Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly
218                    115                   120                   125
219
220    TGG GAC GAG GAC GGC CAC CAC GCA CAG GAT TCA CTC CAC TAC GAA GGC        432
221    Trp Asp Glu Asp Gly His His Ala Gln Asp Ser Leu His Tyr Glu Gly
222            130                   135                   140
223
224    CGT GCC TTG GAC ATC ACC ACG TCT GAC CGT GAC CGT AAT AAG TAT GGT        480
225    Arg Ala Leu Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys Tyr Gly
226    145                   150                   155                   160
227
228    TTG TTG GCG CGC CTA GCT GTG GAA GCC GGA TTC GAC TGG GTC TAC TAC        528
229    Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr
230                    165                   170                   175
231
232    GAG TCC CGC AAC CAC ATC CAC GTA TCG GTC AAA GCT GAT AAC TCA CTG        576
233    Glu Ser Arg Asn His Ile His Val Ser Val Lys Ala Asp Asn Ser Leu
234            180                   185                   190
235
236    GCG GTC CGA GCC GGA GGC TGC TTT CCG GGA AAT GCC ACG GTG CGC TTG        624
237    Ala Val Arg Ala Gly Gly Cys Phe Pro Gly Asn Ala Thr Val Arg Leu
238            195                   200                   205
239
240    CGG AGC GGC GAA CGG AAG GGG CTG AGG GAA CTA CAT CGT GGT GAC TGG        672
241    Arg Ser Gly Glu Arg Lys Gly Leu Arg Glu Leu His Arg Gly Asp Trp
242            210                   215                   220
243
244    GTA CTG GCC GCT GAT GCA GCG GGC CGA GTG GTA CCC ACG CCA GTG CTG        720
245    Val Leu Ala Ala Asp Ala Ala Gly Arg Val Val Pro Thr Pro Val Leu
246    225                   230                   235                   240
247
248    CTC TTC CTG GAC CGG GAT CTG CAG CGC CGC GCC TCG TTC GTG GCT GTG        768
249    Leu Phe Leu Asp Arg Asp Leu Gln Arg Arg Ala Ser Phe Val Ala Val
250                    245                   250                   255
25
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION   *US/09/451,939*

INPUT SET: S34265.raw

Line   Error   Original Text